

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> D6 acetylenase and D6 desaturase from Ceratodon purpureus

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<140> US 09/980,468

<141> 2002-12-03

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<151> 1999-06-07

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<170> PatentIn Vers. 2.0

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 Ala His

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His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
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Gly	Leu	Ile	Glu	Lys	Gly	Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser
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Trp	Ala	Ala	Phe	His	Ile	Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp
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 tgatactctc cccatcattg cttggagtaa agatctcttg gccactgttg agagcaagac 120
 catgttgcca gttcttcagt accagcacct attctttttg gttcttttga cgtttgcccg 180

ggcgagttgg ctatttttga gcgcggcctt cactctcagg cccgagttga cccttggcga 240
gaagcttttg gagaggggaa cgatggcttt gcactacatt tggtttaata gtgttgcggt 300
ttatctgctc cccggatgga aaccagttgt atggatgggtg gtcagcgagc tcatgtctgg 360
tttcctgctg ggatacgtat ttgtactcag tcacaatgga atggaggtgt acaatacgtc 420
aaaggacttc gtgaatgccc agattgcacg gactcgcgac atcaaagcag ggggtgtttaa 480
tgattgggtc accggaggtc tcaacagaca gatt 514

<210> 8

<211> 172

<212> PRT

<213> *Ceratodon purpureus*

<400> 8

Leu	His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	1	5	10	15
Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	20	25	30	
Leu	Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	35	40	45	
His	Leu	Phe	Phe	Leu	Val	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	50	55	60		
Phe	Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	65	70	75	80
Lys	Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	85	90	95	
Ser	Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met	100	105	110	
Val	Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val	115	120	125	
Leu	Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val	130	135	140	
Asn	Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn	145	150	155	160
Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	165	170						

<210> 9

<211> 535

<212> DNA

<213> *Ceratodon purpureus*

<400> 9

tgctcatcac atcgcttgta atagtataga atatgatcca gacctacagt acatccccct 60
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 gccattcgat ggcgtagcac gctctctgat tgcctaccag cactggacgt tttatccaat 180
 aatggctggt gctcgggtga acctctttgc ccaatccctt ctagtactga cctcgaagaa 240
 gcatgtgcc aacaggtggc ttgagctcgg tgctatcggg ttcttctacc tgtgggttctt 300
 caccctcttg tcgtacctgc ccactgcacc ggagagggtt gctttcgtcc ttgtcagttt 360
 tgcagtgaca gggatccagc atgtacagtt ttgcctgaac cacttctcat cgccgggttta 420
 tctaggacag ccgaagagca aggcttgggt tgaatctcaa gcacggggca ctctcaatct 480
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<210> 10

<211> 178

<212> PRT

<213> *Ceratodon purpureus*

<400> 10

Ala	His	His	Ile	Ala	Cys	Asn	Ser	Ile	Glu	Tyr	Asp	Pro	Asp	Leu	Gln	1	5	10	15
Tyr	Ile	Pro	Leu	Phe	Ala	Val	Thr	Ser	Lys	Leu	Phe	Ser	Asn	Leu	Tyr	20	25	30	
Ser	Tyr	Phe	Tyr	Glu	Arg	Val	Met	Pro	Phe	Asp	Gly	Val	Ala	Arg	Ser	35	40	45	
Leu	Ile	Ala	Tyr	Gln	His	Trp	Thr	Phe	Tyr	Pro	Ile	Met	Ala	Val	Ala	50	55	60	
Arg	Val	Asn	Leu	Phe	Ala	Gln	Ser	Leu	Leu	Val	Leu	Thr	Ser	Lys	Lys	65	70	75	80
His	Val	Pro	Asp	Arg	Trp	Leu	Glu	Leu	Gly	Ala	Ile	Gly	Phe	Phe	Tyr	85	90	95	
Leu	Trp	Phe	Phe	Thr	Leu	Leu	Ser	Tyr	Leu	Pro	Thr	Ala	Pro	Glu	Arg	100	105	110	
Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Ala	Val	Thr	Gly	Ile	Gln	His	Val	115	120	125	
Gln	Phe	Cys	Leu	Asn	His	Phe	Ser	Ser	Pro	Val	Tyr	Leu	Gly	Gln	Pro	130	135	140	
Lys	Ser	Lys	Ala	Trp	Val	Glu	Ser	Gln	Ala	Arg	Gly	Thr	Leu	Asn	Leu	145	150	155	160
Ser	Thr	Pro	Ala	Tyr	Met	Asp	Trp	Phe	His	Gly	Gly	Leu	Gln	Phe	Gln				

165

170

175

Ile Glu

<210> 11

<211> 2160

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (159)..(1721)

<400> 11

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tttcgtgggt ttggcgttgg cattgcgcga gggcggacag tgggagtgcg ggaggtctgt 120

ttgtgcatga cgaggtgggt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176
 Met Val Ser Gln Gly Gly
 1 5

ggt ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224
 Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu
 10 15 20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act 272
 Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr
 25 30 35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg 320
 Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr
 40 45 50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368
 Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser
 55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc 416
 Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro
 75 80 85

atc agg cgg agg tgg gtg cag gat aaa aag ccg gtt act tac agc ctg 464
 Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu
 90 95 100

aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc 512
 Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile
 105 110 115

aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga 560
 Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly
 120 125 130

ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc 608
 Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe
 135 140 145 150

tct	act	ttc	cac	gca	tcc	acc	tca	tgg	aag	att	ctt	cag	aat	ttc	tac	656
Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys	Ile	Leu	Gln	Asn	Phe	Tyr	
				155					160					165		
atc	ggg	aac	ctt	ggt	agg	gag	gag	ccg	act	ttg	gag	ctg	ctg	aag	gag	704
Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr	Leu	Glu	Leu	Leu	Lys	Glu	
			170					175					180			
tac	aga	gag	ttg	aga	gcc	ctt	ttc	ttg	aga	gaa	cag	ctt	ttc	aag	agt	752
Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	
		185					190					195				
tcc	aaa	tcc	tac	tac	ctt	ttc	aag	act	ctc	ata	aat	gtt	tcc	att	gtt	800
Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu	Ile	Asn	Val	Ser	Ile	Val	
	200					205					210					
gcc	aca	agc	att	gcg	ata	atc	agt	ctg	tac	aag	tct	tac	cgg	gcg	gtt	848
Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr	Lys	Ser	Tyr	Arg	Ala	Val	
215					220					225					230	
ctg	tta	tca	gcc	agt	ttg	atg	ggc	ttg	ttt	att	caa	cag	tgc	gga	tgg	896
Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Ile	Gln	Gln	Cys	Gly	Trp	
			235						240					245		
ttg	tct	cac	gat	ttt	cta	cac	cat	cag	gta	ttt	gag	aca	cgc	tgg	ctc	944
Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	
			250					255					260			
aat	gac	gtt	gtt	ggc	tat	gtg	gtc	ggc	aac	gtt	gtt	ctg	gga	ttc	agt	992
Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn	Val	Val	Leu	Gly	Phe	Ser	
		265					270					275				
gtc	tcg	tgg	tgg	aag	acc	aag	cac	aac	ctg	cat	cat	gct	gct	ccg	aat	1040
Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	
	280					285					290					
gaa	tgc	gac	caa	aag	tac	aca	ccg	att	gat	gag	gat	att	gat	act	ctc	1088
Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
295					300				305						310	
ccc	atc	att	gct	tgg	agt	aaa	gat	ctc	ttg	gcc	act	gtt	gag	agc	aag	1136
Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu	Ala	Thr	Val	Glu	Ser	Lys	
			315					320					325			
acc	atg	ttg	cga	gtt	ctt	cag	tac	cag	cac	cta	ttc	ttt	ttg	gtt	ctt	1184
Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Leu	Phe	Phe	Leu	Val	Leu	
			330					335					340			
ttg	acg	ttt	gcc	cgg	gcg	agt	tgg	cta	ttt	tgg	agc	gcg	gcc	ttc	act	1232
Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe	Trp	Ser	Ala	Ala	Phe	Thr	
		345					350					355				
ctc	agg	ccc	gag	ttg	acc	ctt	ggc	gag	aag	ctt	ttg	gag	agg	gga	acg	1280
Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys	Leu	Leu	Glu	Arg	Gly	Thr	
	360					365					370					
atg	gct	ttg	cac	tac	att	tgg	ttt	aat	agt	gtt	gcg	ttt	tat	ctg	ctc	1328
Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser	Val	Ala	Phe	Tyr	Leu	Leu	

375	380	385	390	
ccc gga tgg aaa cca gtt gta tgg atg gtg gtc agc gag ctc atg tct				1376
Pro Gly Trp Lys Pro Val Val Trp Met Val Val Ser Glu Leu Met Ser				
	395	400	405	
ggt ttc ctg ctg gga tac gta ttt gta ctc agt cac aat gga atg gag				1424
Gly Phe Leu Leu Gly Tyr Val Phe Val Leu Ser His Asn Gly Met Glu				
	410	415	420	
gtg tac aat acg tca aag gac ttc gtg aat gcc cag att gca tcg act				1472
Val Tyr Asn Thr Ser Lys Asp Phe Val Asn Ala Gln Ile Ala Ser Thr				
	425	430	435	
cgc gac atc aaa gca ggg gtg ttt aat gat tgg ttc acc gga ggt ctc				1520
Arg Asp Ile Lys Ala Gly Val Phe Asn Asp Trp Phe Thr Gly Gly Leu				
	440	445	450	
aac aga .cag att gag cat cat cta ttt cca acg atg ccc agg cac aac				1568
Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn				
	455	460	465	470
ctt aat aaa att tct cct cac gtg gag act ttg tgc aag aag cat gga				1616
Leu Asn Lys Ile Ser Pro His Val Glu Thr Leu Cys Lys Lys His Gly				
	475	480	485	
ctg gtc tac gaa gac gtg agc atg gct tgc ggc act tac cgg gtt ttg				1664
Leu Val Tyr Glu Asp Val Ser Met Ala Ser Gly Thr Tyr Arg Val Leu				
	490	495	500	
aaa aca ctt aag gac gtt gcc gat gct gct tca cac cag cag ctt gct				1712
Lys Thr Leu Lys Asp Val Ala Asp Ala Ala Ser His Gln Gln Leu Ala				
	505	510	515	
gcg agt tga ggcatcgag cactcgctga aacatttttg tctgttatag				1761
Ala Ser				
	520			
tggtcatatg tgatcgaggg gaaaaggtcc catgctctga tctattcttc tgtagccaat				1821
atcttttcaat tgaaaggagg ttcctcactt atcttccatc tatcgttgca catcctgcat				1881
cagagttagc gttggagtaa tgtaagcac ttgtagatta tgcccacat tgccacattt				1941
ctgttcgggtt acaatcgttt gattccatgc tatcctccgt gttcatctcg ttgttataag				2001
caagcttgaa aaaacatgct acgagattgg cagacgttgt cttggcagct gtagaggttg				2061
gttccattca ttgtgtagta cagaactctc tcgtccctgt ttctctacat tacttggtac				2121
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<210> 12

<211> 520

<212> PRT

<213> Ceratodon purpureus

<400> 12

Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn
 1 5 10 15
 Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu
 20 25 30
 Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe
 35 40 45
 Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val
 50 55 60
 Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser
 65 70 75 80
 Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys
 85 90 95
 Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln
 100 105 110
 Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe
 115 120 125
 Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg
 130 135 140
 Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys
 145 150 155 160
 Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr
 165 170 175
 Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg
 180 185 190
 Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu
 195 200 205
 Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr
 210 215 220
 Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe
 225 230 235 240
 Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val
 245 250 255
 Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn
 260 265 270
 Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu
 275 280 285
 His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp
 290 295 300
 Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu

305 310 315 320
 Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His
 325 330 335
 Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe
 340 345 350
 Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys
 355 360 365
 Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
 370 375 380
 Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
 385 390 395 400
 Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
 405 410 415
 Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn
 420 425 430
 Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp
 435 440 445
 Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro
 450 455 460
 Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr
 465 470 475 480
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser
 485 490 495
 Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
 500 505 510
 Ser His Gln Gln Leu Ala Ala Ser
 515 520

<210> 13
 <211> 20
 <212> DNA
 <213> artificial sequence

<220>
 <221> modified_base
 <222> 15
 <223> 15 is inosine

<400> 13

tggtggaart ggamncayaa

<210> 14
 <211> 20

<212> DNA
 <213> artificial sequence
 <220>
 <221> modified_base
 <222> 3, 12, 15
 <223> 3, 12, 15 are inosine
 <400> 14

kgntggaark rnmancaayaa

20

<210> 15
 <211> 20
 <212> DNA
 <213> artificial sequence
 <220>
 <221> 3, 6, 12
 <222> 3, 6, 12 are any nucleotide
 <223> sequencing primer
 <400> 15

atntknggra anarrtgrtg

20

<210> 16
 <211> 18
 <212> DNA
 <213> artificial sequence
 <220>
 <223> sequencing primer
 <400> 16

cgaatgagtg cgacgaac

18

<210> 17
 <211> 18
 <212> DNA
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 <223> sequencing primer
 <400> 17

aataacctgg gctctcac

18

<210> 18
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 <212> DNA
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<220>
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<400> 18

atgaggatat tgatactctc

20

<210> 19
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<212> DNA
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gcaatctggg cattcacg

18

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<400> 20

gacatcaaag ctcttctc

18

<210> 21
<211> 18
<212> DNA
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<220>
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<400> 21

ggc gatgag aagtgggttc

18

<210> 22
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 22

ccggtaccat ggccctcggt accgac

26

<210> 23
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 23

ccgaattctt agtgagcgtg aagccg

26

<210> 24
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 24

ccggtaccat ggtgtcccag ggcggc

26

<210> 25
<211> 26
<212> DNA
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<220>
<223> sequencing primer

<400> 25

ccgaattctc aactcgcagc aagctg

26

<210> 26
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 26

aaaaggatcc aaaatggccc tcggtaccga c

31

<210> 27
<211> 27

21

<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 27

aaaagtcgac ttagtgagcg tgaagcc

27

<210> 28
<211> 60
<212> DNA
<213> artificial sequence

<220>
<223> sequencing primer

<400> 28

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60